



SEQUENCE LISTING

<110> Cahoon, Rebecca E.  
Fang, Yiwen  
Odell, Joan  
Weng, Zude

<120> Plant Myb Transcription Factor Homologs

<130> BB1294 US NA

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<151> 1998-December-02

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 caacaagaag aacagcaagg agccaagacg acgcaacaac gggaccgten acgaccgcca 480  
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 <213> Zea mays

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 Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala  
 35 40 45  
 Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp  
 50 55 60  
 Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly  
 65 70 75 80  
 Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp  
 85 90 95  
 Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys  
 100 105 110  
 Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys  
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20 25 30  
Trp Asp Phe Ile Ala Lys Val Ser Gly Leu Asn Arg Thr Gly Lys Ser  
35 40 45  
Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly  
50 55 60  
Arg Met Ser Pro His Glu Arg Leu Ile Leu Glu Leu His Ala Arg  
65 70 75 80  
Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr  
85 90 95  
Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala  
100 105 110  
Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Ser Leu  
115 120 125  
Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys  
130 135 140  
Gly Gln Glu Leu His Gly Gly Ser Gly Cys Ile Thr Ser Ile Leu Lys  
145 150 155 160  
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Glu Leu Lys

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ggcgcgtgac caccgagagc tgagcggcga cgaggactcc gtggtggcgg ccggagacct 180

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ctgccgcctg cgggtggctca actacctgcg gccggacctg cggcggggca acatcacggc 360
gcaagagcaa ctgctcatcc tggagctgca ctcccgtgg ggcaaccgct ggtcaagatc 420
gcgcagcacc tccaagggca acgacaacga natcanaact actggcgcac cggttcanan 480
caccagcan ctcaatgcaa ctcaaagcan cgctcaagga ctcagcgcta atctggatgc 540
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          20              25              30

Met Leu Leu Val Asn Tyr Val Ala Ala His Gly Glu Gly Arg Trp Asn
          35              40              45

Ala Leu Ala Arg Cys Ala Gly Leu Arg Arg Thr Gly Lys Ser Cys Arg
          50              55              60

Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile
          65              70              75              80

Thr Ala Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly
          85              90              95

Asn Arg Trp Ser Xaa Ile Ala Gln His Leu Gln Gly Gln Arg Gln Arg
          100              105              110

Xaa Xaa Asn Tyr Trp Arg Thr Gly
          115              120

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Ala Ala Gly Leu Lys Arg Thr Gly Lys Xaa Cys Arg Leu Arg Trp Xaa  
35 40 45  
Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Asp Glu  
50 55 60  
Gln Leu Leu Ile Ser Thr Ser His  
65 70

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cagcaaggct gctgcttgct tcccggccgc cgtagcggtc gacgaggagc acggccacca 180
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<213> Zea mays

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 20          25          30

His His Ser His Gln Leu Lys Gly Gly Ala Gln Glu Glu Ala Glu Asn
 35          40          45

Asp Asn Asn Lys Pro Glu Leu Arg Arg Gly Pro Trp Thr Val Asp Glu
 50          55          60

Asp Leu Thr Leu Val Asn Tyr Ile Ala Asp Asn Gly Glu Gly Arg Trp
 65          70          75          80

Asn Asn Leu Ala Arg Ala Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys
 85          90          95

Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn
100         105         110

Phe Ser Ala Asp Glu Gln Leu Leu Ile Leu Asp Leu His Thr Arg Trp
115         120         125

Gly Asn Arg Trp Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp
130         135         140

Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys
145         150         155         160

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Gln Leu Asn Cys Asp Ala Asn Ser Lys Arg Phe Lys Asp Ala Met Arg  
 165 170 175  
 Tyr Leu Trp Met Pro His Leu Ala Asp Asp Val Asp Thr Ile Ala Ala  
 180 185 190  
 Ala Asn Asp Asp Asp Glu Asp His His His Asn Leu Arg Leu Leu Val  
 195 200 205  
 Leu His His His Gln Ala Gln His Leu Gln Gln Ala Ala Ala Ala Ala  
 210 215 220  
 Gly Gly Ala Ala Asn Asp Leu Ala Ala Gly Ala Tyr Asp Val Arg Gln  
 225 230 235 240  
 Leu His Ala Leu Pro Ser Ser Gly Met Ala Ala Thr Ser Ser Ser Asp  
 245 250 255  
 Ser Leu Ala Ser Glu Ser Tyr Asp Asp Gly Gly Leu Leu Phe Ala Asn  
 260 265 270  
 Leu Arg Ala Gly Glu Met Leu Met Asp Gly Gly Asp Trp Ala Ala Gln  
 275 280 285  
 Gln Glu Ala Asp Gln Gly Leu Trp Pro Pro Pro Pro Pro Pro Ser  
 290 295 300  
 Asp Leu Asp Gln Ser Val Val Gln Ala Ala Gly Ala Gly Ala Gly Gln  
 305 310 315 320  
 Phe Gln Asp Met Glu Leu Ser Gly Trp Val Gln Gly Phe Ser Glu Ser  
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 Ile Thr Asp Asn Phe Trp Ala Leu Glu Glu Ile Trp Lys Met Gln  
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 atgtcgatca gatgatgga tgcattcata tgcctgacat agtagatttg atgatatgaa 180  
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<400> 12  
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Ser Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg  
20 25 30

Gly Arg Met Ser Pro Glu Glu Glu Arg Met Val Val Gln Leu His Ala  
35 40 45

Lys Leu Gly Asn Arg Trp Ser Arg Ile Ala Lys Ser Ile Pro Gly Arg  
50 55 60

Thr Asp Asn Glu Ile Lys Asn  
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<210> 13  
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caacaggtgg tctcgcacat ccaagagcat tcctggccgc accgacaacg agatcaagaa 420  
ctactggcgc acccacctgc gcaagctcaa gctcaaacag caaaagcagc agcagtcgga 480  
cgaccaccac aacgacaacg acgacgacga cgaccgcaac tcctcctcct ctctgtcctc 540  
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tggcagcctg caggcccaac atcatgagga ccagcaccaa ctgttccttc atcctctctg 660  
gaacgacgac atcatcgtcg acgtcgactg ctggagcagc agcaccaacg tcgtcgctcc 720  
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Ser Gly Leu Gln Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Val Asn  
35 40 45

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Ser Pro Glu Glu Glu  
50 55 60

Arg Met Val Val Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser Arg  
65 70 75 80



Trp Asp Phe Val Ala Lys Val Ser Gly Leu Arg Gly Leu Asn Arg Thr  
 35 40 45

Gly Lys Ser Cys Arg Leu Arg Trp Val Asn Xaa Leu Gln Pro  
 50 55 60

<210> 17  
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 <213> Oryza sativa

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 gctgaagcgg acggggaaga gctgccggct gcggtggctg aactacctga ggccggacgt 240  
 gaggaggggg aacatgacgg cggaggagca gctgctgata ctggagctcc atgggcggtg 300  
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 ccagcagttc aaggacctca tgcgctacct ctggatgccc gcctcctcga acgcatcaac 480  
 gctcctccca atccaatcca cgacccgacg acccgactct cgtctccgcc gcacactgat 540  
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<210> 18  
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Asp Glu Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu Leu  
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Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ala Leu Ala  
 35 40 45

Arg Cys Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp  
 50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Met Thr Ala Glu  
 65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Gly Arg Trp Gly Asn Arg Trp  
 85 90 95

Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys  
 100 105 110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys His Leu Asn Cys  
 115 120 125

Asp Val Asn Ser Gln Gln Phe Lys Asp Leu Met Arg Tyr Leu Trp Met  
 130 135 140

Pro  
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<210> 19  
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 tcccgatggg gcaaccgatg gtccaagata gcacaacatt tgccctgggag gaccgacgac 180  
 gagatcaaga actactggag gaccagagtg caaaagcatg ccaagcaact caattgtgat 240  
 gtcaacagca agaggttcaa ggatgccatg aagtacctat ggatgcctcg ccttgccgag 300  
 cgcatccatg ccagggtgg cgctgttgat gatagcggag actacagcaa caacgactta 360  
 tcatgtgtat ctggtgtaac aatggccact gttgctaatt gttttgatgg ctctccgagc 420  
 atggtgacta gctcatcctc 440

<210> 20  
 <211> 146  
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 <213> Oryza sativa

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 20 25 30  
 Gln Leu Leu Ile Leu Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser  
 35 40 45  
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asp Glu Ile Lys Asn  
 50 55 60  
 Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Asn Cys Asp  
 65 70 75 80  
 Val Asn Ser Lys Arg Phe Lys Asp Ala Met Lys Tyr Leu Trp Met Pro  
 85 90 95  
 Arg Leu Ala Glu Arg Ile His Ala Arg Ala Gly Ala Val Asp Asp Ser  
 100 105 110  
 Gly Asp Tyr Ser Asn Asn Asp Leu Ser Cys Val Ser Gly Val Thr Met  
 115 120 125  
 Ala Thr Val Ala Asn Cys Phe Asp Gly Ser Pro Ser Met Val Thr Ser  
 130 135 140

Ser Ser  
145

<210> 21  
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<212> DNA  
<213> *Oryza sativa*

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tctatccgat caatcgactg gcccgcgagg atcgatcgag actcgaaagg gagggatttt 180  
gatccggatc ggtcgacgat ggacatggcg cagcagaggg acgcgagcag cgaggaggag 240  
gtgatgggcg gcgacctgcg tcgcggggccg tggacggtgg aggaggacct cctgctcgtc 300  
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aaacgcacag gcaagagctg ccggctccgg tggctgaact acctccgccc cgacctccgg 420  
cgaggcaaca tcacgccgca agagcagctg ctcatcctgg agctgcactc gcggtgggga 480  
aaccgctggt ccaagatngc gcagcacctc ccgggaagca ccgacaacga gatnaagaat 540  
acnggcgcac gcggtgcaga agcacccaag cagtcaagtg cnactcaaca gcaacantta 600  
aggacncatg cgctactcng gatgcccgct ctnnagggat 640

<210> 22  
<211> 115

<212> PRT  
<213> Oryza sativa

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1 5 10 15  
Gly Gly Asp Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu  
20 25 30  
Leu Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ser Leu  
35 40 45  
Ala Arg Ser Ala Xaa Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg  
50 55 60  
Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile Thr Pro  
65 70 75 80  
Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg  
85 90 95  
Trp Ser Lys Xaa Ala Gln His Leu Pro Gly Ser Thr Asp Asn Glu Xaa  
100 105 110  
Lys Asn Thr  
115

<210> 23  
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 ggggccatgg acgccggagg aggacctgat gctggtctcc tacatccagg agcacggcgc 180  
 cggcaactgg cgcgccgtgc cgacgaacac cgggctgatg cgttgacagc agagctgccg 240  
 gctccggtgg acgaactacc tcaggccggg gatcaagcgg gggaacttca ccgagcanga 300  
 ggagaagctc atcgctccacc tccaggctct cctcggcaac cgggtgggcaa cgatnncgtc 360  
 gtacttgccg gganangacg ncaacnacat cangaatact gggaacannc acctcangaa 420  
 gaactcaaga anatgcaagc caccggagggt ggngaaaaca gcgcgncgnc tcgganngtt 480  
 gcgg 484

<210> 24  
 <211> 126  
 <212> PRT  
 <213> Oryza sativa



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 <222> (125)

<400> 24  
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 Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His  
 20 25 30  
  
 Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg  
 35 40 45  
  
 Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
 50 55 60  
  
 Ile Lys Arg Gly Asn Phe Thr Glu Xaa Glu Glu Lys Leu Ile Val His  
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Thr Xaa Xaa Ser Tyr Leu  
85 90 95

Pro Gly Xaa Asp Xaa Asn Xaa Ile Xaa Asn Thr Gly Asn Xaa His Leu  
100 105 110

Xaa Lys Asn Ser Arg Xaa Cys Lys Pro Pro Glu Val Xaa Lys  
115 120 125

<210> 25  
<211> 1427  
<212> DNA  
<213> Oryza sativa

<400> 25  
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tgaagaaggg gccatggacg ccggaggagg acctgatgct ggtctcctac atccaggagc 180  
acggcgccgg caactggcgc gccgtgccga cgaacaccgg gctgatgcgt tgcagcaaga 240  
gctgccggct ccggtggacg aactacctca ggccggggat caagcggggg aacttcaccg 300  
agcaggagga gaagctcatc gtccacctcc aggtctctct cggcaaccgg tgggcagcga 360  
tagcgtcgta cttgccggag aggacggaca acgacatcaa gaactactgg aacacgcacc 420  
tcaagaagaa gctcaagaag atgcaggccg ccggagggtg ggaagacagc ggcgccgct 480  
cggagggtgg cggcgccgcg ggcgacggcg acggcgccgg gaaaagcgtg aaggccgccc 540  
cacctaaggg gcagtgggag cggcggtgc agacggacat ccacacggcg cggcaggcgc 600  
tgcgcgacgc gctctcgctc gaccaccccg acccgtcgcc ggcgacggcg gcggcgccgg 660  
cgacgccagc ggggtcgctc gcggcgtagc cgtcgagcgc ggacaacatc gcgcggctgc 720  
tgcagggttg gatgcgccg ggcgcgccg gcggcgccaa cggcaagggc cccgaggcgt 780  
cgggggtcgac ctccacgacg gcgacgacgc agcagcagcc gcagtgtctc ggcgaggcgc 840  
cggcatccgc gtccgcgtcg gcgagccaga gcggcgccgc cgcgcggcg actgccaga 900  
cgccggagtg ctcgacggag acgagcaaga tggccaccgg cggcgccgcc ggcgcccccg 960  
cgccggcggt ctcgatgctg gagagctggc tgctcgacga cggcgccatg gggctcatgg 1020  
acgtggtgcc attgggggac cccagtgagt tcttttaagt gtagtacaac caaaattaaa 1080  
ttaatcaagt agacagcaag aaaaaaaaaa aataatggaa agttgccgag ttaattaatc 1140  
aagatgcaac taatcaaagc taattaaaag ggcttcgagt taattctcgg tgattttaat 1200  
cgagtttgca ggtgttgatc tagcttggtt aattaatcct ttcttttgta ggtttttagt 1260  
taattagtct ctctgatgat gctagggttt ggaactgac atagttaagt taatttatac 1320  
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gtacatcttt ttaaaaagata aaaaaaaaaa aaaaaaaaaa aaaaaaa 1427

<210> 26  
<211> 323  
<212> PRT  
<213> Oryza sativa

<400> 26  
Met Gly Arg Pro Pro Cys Cys Asp Lys Val Gly Val Lys Lys Gly Pro  
1 5 10 15

Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His  
20 25 30

Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg  
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Leu Ile Val His  
 65 70 75 80  
 Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu  
 85 90 95  
 Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu  
 100 105 110  
 Lys Lys Lys Leu Lys Lys Met Gln Ala Ala Gly Gly Gly Glu Asp Ser  
 115 120 125  
 Gly Ala Ala Ser Glu Gly Gly Gly Gly Arg Gly Asp Gly Asp Gly Gly  
 130 135 140  
 Gly Lys Ser Val Lys Ala Ala Ala Pro Lys Gly Gln Trp Glu Arg Arg  
 145 150 155 160  
 Leu Gln Thr Asp Ile His Thr Ala Arg Gln Ala Leu Arg Asp Ala Leu  
 165 170 175  
 Ser Leu Asp His Pro Asp Pro Ser Pro Ala Thr Ala Ala Ala Ala Ala  
 180 185 190  
 Thr Pro Ala Gly Ser Ser Ala Ala Tyr Ala Ser Ser Ala Asp Asn Ile  
 195 200 205  
 Ala Arg Leu Leu Gln Gly Trp Met Arg Pro Gly Gly Gly Gly Gly Gly  
 210 215 220  
 Asn Gly Lys Gly Pro Glu Ala Ser Gly Ser Thr Ser Thr Thr Ala Thr  
 225 230 235 240  
 Thr Gln Gln Gln Pro Gln Cys Ser Gly Glu Gly Ala Ala Ser Ala Ser  
 245 250 255  
 Ala Ser Ala Ser Gln Ser Gly Ala Ala Ala Ala Ala Thr Ala Gln Thr  
 260 265 270  
 Pro Glu Cys Ser Thr Glu Thr Ser Lys Met Ala Thr Gly Gly Gly Ala  
 275 280 285  
 Gly Gly Pro Ala Pro Ala Phe Ser Met Leu Glu Ser Trp Leu Leu Asp  
 290 295 300  
 Asp Gly Gly Met Gly Leu Met Asp Val Val Pro Leu Gly Asp Pro Ser  
 305 310 315 320  
 Glu Phe Phe

<210> 27  
 <211> 557  
 <212> DNA  
 <213> Glycine max  
  
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 <222> (552)..(553)

<400> 27  
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 agaagacttg atcttngatc aactatattg caaatcatgg ggaaggtggt tggaattctt 180

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tggccaaaag ctgctggtct caaacgtacc ggaaagattg cgggctaang tggctaaaact 240
acctccgtcc tgatgttaga agagggaata ntacacccga aggaacaact ttgatcatgg 300
agcttcacgc aaagtgggga aacaggtggt ccaaaattgc caagcatcta cctggtagga 360
cagtaatgag atnaagaact antggnggac aaggatcaga agcacatcaa gcaactgaga 420
attnagcaac aatcacataa ctctgagata atgttacaag ctagatacca agttntacaa 480
ggtgaaccat ggnnactatc ccaacctttt naaggaagtn angcatttct naatcnttcc 540
ccaaataacc gnntatc 557

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<210> 28
<211> 94
<212> PRT
<213> Glycine max

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<220>
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<220>
<221> UNSURE
<222> (51)

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<220>
<221> UNSURE
<222> (65)

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<400> 28
Ser Gln Asp Pro Glu Val Arg Lys Gly Pro Trp Thr Met Glu Glu Asp
 1             5             10             15

Leu Ile Xaa Xaa Ile Asn Tyr Ile Ala Asn His Gly Glu Gly Val Trp
      20             25             30

Asn Ser Leu Ala Lys Ser Cys Trp Ser Gln Thr Tyr Arg Lys Asp Cys
      35             40             45

Arg Leu Xaa Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn
 50             55             60

Xaa Thr Pro Glu Gly Thr Thr Leu Ile Met Glu Leu His Ala Lys Trp
 65             70             75             80

Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr
      85             90

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<210> 29
<211> 988
<212> DNA
<213> Glycine max

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<400> 29
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atggataaaa aacaactgtg caacacgtct caagatcctg aagtgagaaa aggaccttgg 120
acgatggaag aagacttgat cttgatcaac tatattgcaa atcatgggga aggtgtttgg 180
aattcttttg ccaaagctgc tggctctcaa cgtaccggaa agagttgccg gctaagggtg 240
ctaaactacc tccgtcctga tgttagaaga gggaatatta caccgagga acaacttttg 300
atcatggagc ttcacgcaaa gtgggggaaac aggtgggtcca aaattgccaa gcatctacct 360
ggtaggacag ataatgagat caagaactat tggaggacca ggatccagaa gcacatcaag 420
caagctgaga actttcagca acaaactcagc aataactctg agataaatga tcaccaagct 480
agcactagcc atgtttctac catggctgaa cccatggaga cctattctcc acccttttat 540
caaggaatgt tagagccatt ttcttcaatt cagttcccca caattaatcc tgatcaatcc 600

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agttgttgta ccaatgacaa caacaacagc attaactatt ggagcatgga ggatatctgg 660
tcaatgcagt tactgaacgg ggattaaata ttgatataac aagataaacc taaattcttg 720
tataagttcc ataaaacact ggaatgtctc tggcttaaaa catattatta ttaggtttgt 780
ttatataagt agttggatat gtttggtttt gcgtaccatt attagcatat atatatatat 840
ttcaaagtga atgctatgtg cattgtaaaa gatatggtta agaaccacat agtttcaaaa 900
ctcttaaata taattccagt cacttattat aggaagtcta ttattaatta tctccaagat 960
gtttgcttaa aaaaaaaaaa aaaaaaaaaa 988

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<210> 30
<211> 208
<212> PRT
<213> Glycine max

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<400> 30
Met Asp Lys Lys Gln Leu Cys Asn Thr Ser Gln Asp Pro Glu Val Arg
 1          5          10          15

Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile
      20          25          30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
      35          40          45

Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
 50          55          60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
 65          70          75          80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
      85          90          95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
      100          105          110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
      115          120          125

Ile Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
      130          135          140

Val Ser Thr Met Ala Glu Pro Met Glu Thr Tyr Ser Pro Pro Phe Tyr
      145          150          155          160

Gln Gly Met Leu Glu Pro Phe Ser Ser Ile Gln Phe Pro Thr Ile Asn
      165          170          175

Pro Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ser Ile Asn
      180          185          190

Tyr Trp Ser Met Glu Asp Ile Trp Ser Met Gln Leu Leu Asn Gly Asp
      195          200          205

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<210> 31
<211> 530
<212> DNA
<213> Glycine max

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 tggaaactctt tggccaaggc tgctggactt aaacgtaccg gaaagagttg ccggctccgg 180  
 tggctaaact acctccgtcc tgatgttaga agaggggaata ttacacccga ggaacagctt 240  
 ttgatcatgg aacttcatgc aaagtgggga aacagggtggt ccaaaaattgc caagcatcta 300  
 nccggaagga ctgataatga gattaagaac tactggagga caaggatcaa gaacantca 360  
 agcaagcctt caacaacttc aacaacanag tantaattct gagataattt acatcccaag 420  
 cttgcacaac caattgtcaa caatgggcaa cccaaaaaaa ctaatctcan caatttcaag 480  
 gaagnttatt cattnaatca attccaaaaa ccncacntct antgtttcaa 530

<210> 32  
 <211> 204  
 <212> PRT  
 <213> Glycine max

<400> 32  
 Met Asp Lys Lys Leu Gly Asn Thr Ser His Asp Pro Glu Val Arg Lys  
 1 5 10 15

Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Thr Tyr Ile Ala  
                     20                    25                    30  
 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu  
                     35                    40                    45  
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg  
                     50                    55                    60  
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile  
                     65                    70                    75                    80  
 Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys  
                     85                    90                    95  
 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr  
                     100                    105                    110  
 Arg Ile Gln Lys His Leu Lys Gln Ala Ser Ser Ser Phe Gln Gln Gln  
                     115                    120                    125  
 Ser Ser Asn Ser Glu Ile Ile Tyr His Pro Gln Ala Cys Thr Ser Gln  
                     130                    135                    140  
 Val Ser Thr Met Ala Gln Pro Ile Glu Thr Tyr Ser Pro Pro Ser Tyr  
                     145                    150                    155                    160  
 Gln Gly Met Leu Asp Pro Phe Ser Ile Gln Phe Pro Thr Asn Pro His  
                     165                    170                    175  
 His Ser Ser Cys Cys Thr Asn Asp Asp Asp Asn Asn Asn Tyr Trp Ser  
                     180                    185                    190  
 Met Glu Asp Ile Trp Ser Met Gln Leu Ala Asn Tyr  
                     195                    200

<210> 33  
 <211> 910  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
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 aactatattg caaatcacgg tgaagggtgt tggaaattctt tagccaaagc ttctgggtctt 180  
 aaacgaacgg gaaagagttg tcgactccgt tggctaaact accttcgtcc tgatgttaga 240  
 agaggaaaca ttacacccga agaacagctt ttgatcatag aacttcatgc aaagtggggc 300  
 aataggtggt ccaaaattgc aaagcatctt ccaggaagaa ctgacaatga gattaagaac 360



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ttctggagaa ctaggatcca gaagcacatt aagcaagctg agacttcaca acaacatggt 420
aattcatcag agaatagtaa taatgatcat caagcaagca atagcactag caagggtgtcc 480
accatggcac atccaaatga gactttctct tcaccctcat accaagcaac ttttgagcca 540
tttcaacctc aattcctaca atcaatgatc aatcaagttg ttgtaccagc aacaacaact 600
attggagcat cgaggatata tggtcgtcta tgcaattact caatggagat waattaaatc 660
tagctatatg catgcttata taaatcatat atgtgatgat atataaacct aagctcttat 720
tgagtgtggt caggcttaat aacatcatta ggtctggtat atatgagtag gttaagattg 780
gtgtgcatgc ctaaatgnag tattgcntta ttgnagtaag aataactagt tatggatgcc 840
tttaaaaaaa agttagttat gaattgaaat atatagtaac ttatatacta aaaaaaaaaa 900
aaaaaaaaaa                                     910

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<210> 34
<211> 206
<212> PRT
<213> Glycine max

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<400> 34
Met Asp Lys Lys Pro Cys Asp Ser Ser His Asp Pro Glu Val Arg Lys
 1          5          10          15

Gly Pro Trp Ile Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
      20          25          30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu
      35          40          45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
      50          55          60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
      65          70          75          80

Ile Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
      85          90          95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
      100          105          110

Arg Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly
      115          120          125

Asn Ser Ser Glu Asn Ser Asn Asn Asp His Gln Ala Ser Asn Ser Thr
      130          135          140

Ser Lys Val Ser Thr Met Ala His Pro Asn Glu Thr Phe Ser Ser Pro
      145          150          155          160

Ser Tyr Gln Ala Thr Phe Glu Pro Phe Gln Pro Gln Phe Leu Gln Ser
      165          170          175

Met Ile Asn Gln Val Val Val Pro Ala Thr Thr Thr Ile Gly Ala Ser
      180          185          190

Arg Ile Ser Gly Arg Leu Cys Asn Tyr Ser Met Glu Ile Asn
      195          200          205

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<210> 35
<211> 863
<212> DNA
<213> Glycine max

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<400> 35
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agatcctgaa gtgagaaaag ggccttggac aatggaagaa gacttgatct tgatgaacta 120
tattgcaaat catggggaag gtgtttggaa ctctttggcc aaagctgctg gtctcaaacg 180
taacggaaaag agttgccggc taagggtggct aaattacctc cgtcctgatg ttagaagagg 240
gaatattaca cccgaggaac aacttttgat tatggagctc cacgcaaagt ggggaaacag 300
gtgggtccaaa attgccaaag atctacctgg aaggactgat aatgagatca agaactattg 360
gaggacaagg atccagaagc acatcaagca agctgagaac tttcagcaac agagtagtaa 420
taattctgag ataaatgata accaagctag cactagccat gtttccacca tggctgagcc 480
catggagatg tattctccac cctgttatca aggaatgtta gagccatttt caactcagtt 540
ccctacaatt aatcctgatc aatccagttg ttgtaccaat gacaacaaca acattaacta 600
ttggagcatg gaggatagct ggtcaatgca attactgaac ggtgattaaa tattatcaag 660
ataaaaccta agttytgaag ttccataagg ctggaatgtc tytgatttaa aacatattat 720
tgggtttgtt tatataagta gttggatgtt tggttttgcg taccattatt agctatgtgc 780
tgtaatatat acgagatytt atattaaact atatctgcat gctttatata taaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa aaa 863

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<210> 36
<211> 206
<212> PRT
<213> Glycine max

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<400> 36
Met Asp Lys Lys Gln Gln Cys Lys Thr Ser Gln Asp Pro Glu Val Arg
 1          5          10          15

Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Met Asn Tyr Ile
      20          25          30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
      35          40          45

Leu Lys Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
      50          55          60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
      65          70          75          80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
      85          90          95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
      100          105          110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
      115          120          125

Ser Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
      130          135          140

Val Ser Thr Met Ala Glu Pro Met Glu Met Tyr Ser Pro Pro Cys Tyr
      145          150          155          160

Gln Gly Met Leu Glu Pro Phe Ser Thr Gln Phe Pro Thr Ile Asn Pro
      165          170          175

Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ile Asn Tyr Trp
      180          185          190

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Ser Met Glu Asp Ser Trp Ser Met Gln Leu Leu Asn Gly Asp  
 195 200 205

<210> 37  
 <211> 805  
 <212> DNA  
 <213> Glycine max

<400> 37  
 aaaaaacccat gcaactcatc atctcatgat cctgaagtga gaaagggacc atggaccatg 60  
 gaagaagact tgatcttgat aaactatat gcaaatcacg gtgaagggtgt ttggaactcc 120  
 ttagccaaag cttctgggtct caaacgaacg ggaaagagtt gtcgactccg ttggctaaac 180  
 taccttcgtc ctgatgttag aagaggaaac attacaccg aggaacagct tttgatcata 240  
 gaacttcacg caaagtggg caataggtgg tccaaaattg caaagcatct tccaggaaga 300  
 actgacaatg agattaagaa cttctggaga acaaggatcc aaaagcacat taagcaagct 360  
 gagacttcac aacaacatgg taattcagag aataatgatc atcaagcaag cactagtact 420  
 agcaaagtgt ccaccatggc acatccaaat gagactttct ctccaccctc ataccaagga 480  
 acttttgagc cattccaacc tcaattccct acaatcactg atcaatcaag ttgttggtacc 540  
 accaccaacg acaacaacaa ctattggagc atcgaggata tctggtcgtc tatgcaatta 600  
 ctcaatggag attaaacctta gctatatgca tgcctatata aatcatatat atgatgatat 660  
 ataaacctaa gctctttag agtgtgttca ggcttaataa catcattagg tctgtttata 720  
 tgagtagtct aagtttggtg tttgtaatgc atgatgtgag ttaagaatta atttagttat 780  
 ggttggaata aaaaaaaaaa aaaaa 805

<210> 38  
 <211> 204  
 <212> PRT  
 <213> Glycine max

<400> 38  
 Lys Lys Pro Cys Asn Ser Ser Ser His Asp Pro Glu Val Arg Lys Gly  
 1 5 10 15  
 Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala Asn  
 20 25 30  
 His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu Lys  
 35 40 45  
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro  
 50 55 60  
 Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile Ile  
 65 70 75 80  
 Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys His  
 85 90 95  
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr Arg  
 100 105 110  
 Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly Asn  
 115 120 125  
 Ser Glu Asn Asn Asp His Gln Ala Ser Thr Ser Thr Ser Lys Val Ser  
 130 135 140  
 Thr Met Ala His Pro Asn Glu Thr Phe Ser Pro Pro Ser Tyr Gln Gly  
 145 150 155 160

Thr Phe Glu Pro Phe Gln Pro Gln Phe Pro Thr Ile Thr Asp Gln Ser  
165 170 175

Ser Cys Cys Thr Thr Thr Asn Asp Asn Asn Asn Tyr Trp Ser Ile Glu  
180 185 190

Asp Ile Trp Ser Ser Met Gln Leu Leu Asn Gly Asp  
195 200

<210> 39  
<211> 751  
<212> DNA  
<213> Glycine max

<400> 39  
tggatgttaa gaaaggtggg tctgtagtac aagcacaagt gaagttgcag aagcataacg 60  
aaaaggagat gggcatgaga aaaggtccat gggcggttga ggaggacacc attctggtca 120  
attacatcgc cacacacggt gaaggccact ggaattccgt ggcacgatgt gcaggtctaa 180  
ggaggagtgg gaagagttgc agattaaggt ggctaaacta cttgcgcccc gacgtgcggc 240  
gtggaaatat cacactccaa gaacaaatat taattctcga ccttcaactct cgctggggca 300  
acaggtggtc aaagattgct caacagctgc caggaagaac agacaacgaa ataaagaact 360  
attggaggac cagagtgata aaacaagcga agcagctaaa gtgcgatgtg aatagcaaac 420  
agttcagaga cacgttgctg tacgttttga tgccgcgctt gctggagcgg cttcagcccc 480  
catcacaagc actggagcca aaccaaagtg gacttggtt acacgcttca tcatcactgc 540  
ttccttcgaa ttccgaccat agtattgaaa gggggtcgga tctgtggcca ggtttcaata 600  
accaaagtgt gttggaacag gggagtggcg gtgacttggt ggaaagttt tgggatgacg 660  
acaatatgtg ctttttgcaa cagctttctt atgacctcca aatgaaataa aatacaattc 720  
ccttccgtca cgcaaaaaaa aaaaaaaaaa a 751

<210> 40  
<211> 235  
<212> PRT  
<213> Glycine max

<400> 40  
Asp Val Lys Lys Gly Gly Ser Val Val Gln Ala Gln Val Lys Leu Gln  
1 5 10 15

Lys His Asn Glu Lys Glu Met Gly Met Arg Lys Gly Pro Trp Ala Val  
20 25 30

Glu Glu Asp Thr Ile Leu Val Asn Tyr Ile Ala Thr His Gly Glu Gly  
35 40 45

His Trp Asn Ser Val Ala Arg Cys Ala Gly Leu Arg Arg Ser Gly Lys  
50 55 60

Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg  
65 70 75 80

Gly Asn Ile Thr Leu Gln Glu Gln Ile Leu Ile Leu Asp Leu His Ser  
85 90 95

Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Gln Leu Pro Gly Arg  
100 105 110

Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Ile Lys Gln  
115 120 125

Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Lys Gln Phe Arg Asp Thr  
130 135 140

Leu Arg Tyr Val Trp Met Pro Arg Leu Leu Glu Arg Leu Gln Pro Thr  
145 150 155 160

Ser Gln Ala Leu Glu Pro Asn Gln Ser Gly Leu Val Leu His Ala Ser  
165 170 175

Ser Ser Leu Leu Pro Ser Asn Ser Asp His Ser Ile Glu Arg Gly Ser  
180 185 190

Asp Leu Trp Pro Gly Phe Asn Asn Gln Met Leu Leu Glu Gln Gly Ser  
195 200 205

Gly Gly Asp Leu Leu Glu Ser Leu Trp Asp Asp Asp Asn Met Cys Phe  
210 215 220

Leu Gln Gln Leu Ser Tyr Asp Leu Gln Met Lys  
225 230 235

<210> 41  
<211> 500  
<212> DNA  
<213> Glycine max

<400> 41  
catttctaata tgttctgata catatatata atacttttctt tgtaataact taaagaaccc 60  
cacaaaaaca ccaaccatgt ccacaattgc aaagagagat ttgagttcta atgaagaaga 120  
gagtgaagctg agaagaggct cttggactct tgaagaagac agcttactca tacactatat 180  
tgctcgatcat ggtgaaggcc gttggaatat gttagccaaa agtgcaggat tgaagaggac 240  
tggaaaaagt tgcagactta gatggctgaa ttatttgaaa ccagacatta agagagggaa 300  
cctcaactcca caggagcaac tcttgatcct tgaactccat tccaagtggg gtaacaggtg 360  
gtcaaaaatt gctcagcatc tgccaggaag aacagacaat gagatcaaga actattggag 420  
aacaaggata cagaaacagg gcacgccaac ttaacattga atctggtagc aagagattca 480  
ttgatgctgt cagtgttttt 500

<210> 42  
<211> 229  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (138)

<400> 42  
Met Ser Thr Ile Ala Lys Arg Asp Leu Ser Ser Asn Glu Glu Glu Ser  
1 5 10 15

Glu Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Ser Leu Leu Ile  
20 25 30

His Tyr Ile Ala Arg His Gly Glu Gly Arg Trp Asn Met Leu Ala Lys  
35 40 45

Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu  
50 55 60

Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly Asn Leu Thr Pro Gln Glu  
 65 70 75 80  
 Gln Leu Leu Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser  
 85 90 95  
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn  
 100 105 110  
 Tyr Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg Gln Leu Asn Ile Glu  
 115 120 125  
 Ser Gly Ser Lys Arg Phe Ile Asp Ala Xaa Lys Cys Phe Trp Met Pro  
 130 135 140  
 Arg Leu Leu Gln Lys Met Glu Gln Ser Asn Ser Pro Ser Pro His His  
 145 150 155 160  
 Ser Ser Met Thr Asn Met Met Asn Leu Gly Asn Ser Gly Glu Ala Ser  
 165 170 175  
 Met Ser Ser Met Ser Ser Ser Phe Asn Ile Asn Pro Ser Met Ser Ser  
 180 185 190  
 Ser Ser Ser Pro Pro Lys Gly Asn Leu Leu Trp Met Met Pro Asn His  
 195 200 205  
 Phe Lys Tyr Tyr Val Gln Pro His Gln Ser Ile Pro Arg Phe Leu Pro  
 210 215 220

Ile Phe Thr Ala Thr  
225

<210> 43  
 <211> 1348  
 <212> DNA  
 <213> Glycine max

<400> 43  
 tacctctcca accaagacca atttgaaaac ctcttcaatc caacaaacaa acgttctccc 60  
 ttttgttctg agagaatcaa tggatggaaa aggagcaaga agtagcaaca cccttttaag 120  
 tagtgaggac gagatggacc ttcgaagagg cccttggacc gtcgatgaag acctcactct 180  
 tatcaattac gttgccactc atggcggaagg tcgctggaat accctcgccc tctctgctgg 240  
 gctgaaacga acggggaaga gttgcagatt gaggtggctg aattatctgc gtccctgatgt 300  
 tcgacgtgga aacatcacgc ttgaagaaca acttttgatt ctggagctcc attctcgctg 360  
 gggaaaccga tggtcgaaaa ttgctcaata tttgcctggt agaaccgaca atgagataaa 420  
 gaactattgg agaaccctgt tccaaaagca tgccaagcaa ctcaaatgcg acgtgaatag 480  
 caagcaattc aaggacacca tgcgttacat ttggatgcca aggctcgtgg aacgcattca 540  
 agccaccgct gccgcctccg caccacaacc cgttaccgta ccaccgagac caacaatgca 600  
 tacacctacg gaagcaacct taataacaac aaattcgagg ttacgatca caagggcaaa 660  
 atgggggttaa ccgatccttc agttatgaac aatgacttaa tgggttcaca tgtcacgcaa 720  
 agttacaccc ctgagaatag tagcaccggt gcgtcatcat cagactcgtt tgggactcaa 780  
 gtctcagcaa tttctgattt gactgaatat tacactgtca ctggtagtgg taacaataac 840  
 aatactaatt ctgcggatta ttatcaaccc tctcaaatta gttactcgga tagttgcatc 900  
 acaagcccat ctgggttggt ccccaagggt ctagattttc aatccatgga tccaaacacc 960  
 ccgtggaaca tgcgaagtgg ggactcctct gacagttttt ggaacgttga aagcatgttg 1020  
 ttcttagagc agcaactcat gaatgacaac atgtgaaaac attgggaata ggaaaataag 1080  
 acttagatac ggttcttctt agtattgtgt tttaattaaa gttaaagtta acacaagtta 1140  
 ttgaagtga actttaattt taattgaata ataatactga aaacaagagt tgtattttaag 1200  
 ttttattctt ttatgaatta tgaattagat tgacagaagg gggtgtttgt gaaatataca 1260

ggtgaaagta tagaaagtag caacattaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1348

<210> 44  
 <211> 196  
 <212> PRT  
 <213> Glycine max

<400> 44  
 Met Asp Gly Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Ser Glu  
     1                    5                    10                    15  
 Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu  
                     20                    25                    30  
 Thr Leu Ile Asn Tyr Val Ala Thr His Gly Glu Gly Arg Trp Asn Thr  
                     35                    40                    45  
 Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu  
                     50                    55                    60  
 Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr  
                     65                    70                    75                    80  
 Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn  
                     85                    90                    95  
 Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu  
                     100                    105                    110  
 Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu  
                     115                    120                    125  
 Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Arg Tyr Ile  
                     130                    135                    140  
 Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala Thr Ala Ala Ala Ser  
                     145                    150                    155                    160  
 Ala Pro Gln Pro Val Thr Val Pro Pro Arg Pro Thr Met His Thr Pro  
                     165                    170                    175  
 Thr Glu Ala Thr Leu Ile Thr Thr Asn Ser Arg Phe Thr Ile Thr Arg  
                     180                    185                    190  
 Ala Lys Trp Gly  
                     195

<210> 45  
 <211> 1236  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (519)

<220>  
 <221> unsure  
 <222> (521)

<220>  
 <221> unsure  
 <222> (530)..(531)

<220>  
 <221> unsure  
 <222> (534)

<220>  
 <221> unsure  
 <222> (800)

<220>  
 <221> unsure  
 <222> (1124)

<220>  
 <221> unsure  
 <222> (1151)

<400> 45  
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 aaacttaatt tcttttgttt tgagtttctt agagaatgga tgaaaaagga gcaagaagta 120  
 gcaacaccct tttaagttgt gaggacgaga tggaccttcg aagaggccct tggaccgtcg 180  
 atgaagacct cactcttatt aattacattg ccactcatgg cgaaggctgc tggaacacgc 240  
 tcgccctctc tgctgggctg aaacgaacgg ggaagagttg cagattgagg tggctgaatt 300  
 atctgcgtcc tgatgttcga cgtggaaaca tcacacttga agaacaactt ttgattcttg 360  
 agcttcattc tcgctgggga aaccgttggt cgaaaattgc tcaatatattg cctggtagaa 420  
 ccgacaacga gataaagaac tattggagaa cccgtgtcca aaagcatgcc aagcaactca 480  
 aatgtgacgt gaatagcaag caattcaagg acaccatgng ntacctttgn natnccaagg 540  
 ctcggtggaac gcattcaagc agcggcgacg gccccgtaa ccaccacgt aactgcggcc 600  
 gccaccaaca atgcattcac ctacggraac aaccttatac caccaaattc gaggttctga 660  
 atcacaaggg cagaatgggg ttaaccgatc cttcagttgc gaacaatgac tttgtgggtt 720  
 cacatgtcac gcaaaggtag cctactcctg agaatagtag cacgggtgcg tcatcatcag 780  
 actcgtttgg gactcaagtn tcaacaattt ctgatttgac tgaaaattcc agtgtccctg 840  
 aaaatactaa ttctgcggat tattatcaac cctctcaaat tagtaattac tcggataatt 900  
 gcatcacaag cccatctggg ttcttgttcc ctcaaggact agatcttcaa tccatggatc 960  
 caaacacacc gtggaacatg caaagtgggg actcctctga caatttttgg gacgttgaaa 1020  
 gcatgttatt cttagagcag caactcatga atgacaacat gtgaaacatt gggaaatagga 1080  
 aaataagact tagatacgtt tcttctaata ttttttagtg ktgngtttta attaaagtta 1140  
 aagttaacac nagttattga agtgaaactt taattttaat taaataataa tcctgaaaaa 1200  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1236

<210> 46  
 <211> 322  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (142)

<220>  
 <221> UNSURE  
 <222> (145)..(146)..(147)

<220>  
 <221> UNSURE  
 <222> (178)



<400> 46  
Met Asp Glu Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Cys Glu  
1 5 10 15  
Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu  
20 25 30  
Thr Leu Ile Asn Tyr Ile Ala Thr His Gly Glu Gly Arg Trp Asn Thr  
35 40 45  
Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu  
50 55 60  
Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr  
65 70 75 80  
Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn  
85 90 95  
Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu  
100 105 110  
Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu  
115 120 125  
Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Xaa Tyr Leu  
130 135 140  
Xaa Xaa Xaa Lys Ala Arg Gly Thr His Ser Ser Ser Gly Asp Gly Pro  
145 150 155 160  
Arg Asn His His Arg Asn Cys Gly Arg His Gln Gln Cys Ile His Leu  
165 170 175  
Arg Xaa Gln Pro Tyr Thr Thr Lys Phe Glu Val Leu Asn His Lys Gly  
180 185 190  
Arg Met Gly Leu Thr Asp Pro Ser Val Ala Asn Asn Asp Phe Val Gly  
195 200 205  
Ser His Val Thr Gln Arg Tyr Pro Thr Pro Glu Asn Ser Ser Thr Gly  
210 215 220  
Ala Ser Ser Ser Asp Ser Phe Gly Thr Gln Val Ser Thr Ile Ser Asp  
225 230 235 240  
Leu Thr Glu Asn Ser Ser Val Pro Glu Asn Thr Asn Ser Ala Asp Tyr  
245 250 255  
Tyr Gln Pro Ser Gln Ile Ser Asn Tyr Ser Asp Asn Cys Ile Thr Ser  
260 265 270  
Pro Ser Gly Phe Leu Phe Pro Gln Gly Leu Asp Leu Gln Ser Met Asp  
275 280 285  
Pro Asn Thr Pro Trp Asn Met Gln Ser Gly Asp Ser Ser Asp Asn Phe  
290 295 300

Trp Asp Val Glu Ser Met Leu Phe Leu Glu Gln Gln Leu Met Asn Asp  
 305 310 315 320

Asn Met

<210> 47  
 <211> 1181  
 <212> DNA  
 <213> Glycine max

<400> 47  
 tttcagtgag tgagaatagc catgtctact tcaaagagcg tcagcagttc tagtgaagat 60  
 gacaatgaac ttagaagagg gccttggaact ctggaagagg ataacttgct ctcccaatat 120  
 atttttaatc atggggaagg gcgatggaat ttgctggcta aacgttcagg attaaagaga 180  
 actgggaaaa gttgcagatt aaggtggcta aattatctaa agccagatgt aaaacgggga 240  
 aatttaaccc cacaagagca acttataatt cttgaactcc actcaaagtg gggaaacagg 300  
 tgggtcaaaaa ttgcacaaca tttgccaggc agaacagaca atgaaatcaa gaactattgg 360  
 agaactagga ttcagaaaaca agcaagacat ttgaaaattt acaactgacag cagagagttt 420  
 caagaacttg ttaggcgttt ctggatgcct agattgcttc agaaagcaaa agaatcatct 480  
 tcttcaaaca tgtcaattca aaaccaggca attcctatgc cttttgatta tgtttctcag 540  
 catttaactg ttgggaccat acctccttg cagggacctt gtatgaatga agctgggtccc 600  
 acttacatgg accaacaatga gcagactcag actcggaaca ccaacaatgg ttcatgcac 660  
 tccttgctctg agtcagcaaa tattccaaaa gtgcctcagc attttggaca caccaccatc 720  
 acccaatttc atgccttgaa taccaatgac tttggcacct tcacatatga aggttataat 780  
 gtaaacacaa atgtctatga gatggacaac ttcaaaacga ctactacatg ggtggctgag 840  
 gatgcgcaat acccaattgg tgattgtcaa atggtaggaa gcaattgggt aaacaacgat 900  
 tttgcatgta acatgtggaa catggatgaa ctgtggcagt ttagcaagtt acaaaaaataa 960  
 gatttttaggg ttttgttttt tttggaataa ccaaaagtcc aaaactcttt ctttgatgac 1020  
 gttattattg ttatcatgaa ctgtggatta gctaccgaat taattaatac agatggcgat 1080  
 tgttttctgt acatctgtct tgtattactc tgttcagata agtacttttg taatttgtat 1140  
 tgattgagaa aagtcattaa ttagtcacta gtacaaaaaa a 1181

<210> 48  
 <211> 312  
 <212> PRT  
 <213> Glycine max

<400> 48  
 Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu  
 1 5 10 15  
 Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln  
 20 25 30  
 Tyr Ile Phe Asn His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg  
 35 40 45  
 Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn  
 50 55 60  
 Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln  
 65 70 75 80  
 Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys  
 85 90 95  
 Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
 100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Tyr Thr  
 115 120 125  
 Asp Ser Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg  
 130 135 140  
 Leu Leu Gln Lys Ala Lys Glu Ser Ser Ser Ser Asn Met Ser Ile Gln  
 145 150 155 160  
 Asn Gln Ala Ile Pro Met Pro Phe Asp Tyr Val Ser Gln His Leu Thr  
 165 170 175  
 Val Gly Thr Ile Pro Pro Trp Gln Gly Pro Cys Met Asn Glu Ala Gly  
 180 185 190  
 Pro Thr Tyr Met Asp Gln His Glu Gln Thr Gln Thr Arg Asn Thr Asn  
 195 200 205  
 Asn Gly Ser Cys Ile Ser Leu Ser Glu Ser Ala Asn Ile Pro Lys Val  
 210 215 220  
 Pro Gln His Phe Gly His Thr Thr Ile Thr Gln Phe His Ala Leu Asn  
 225 230 235 240  
 Thr Asn Asp Phe Gly Thr Phe Thr Tyr Glu Gly Tyr Asn Val Asn Asn  
 245 250 255  
 Asn Val Tyr Glu Met Asp Asn Phe Lys Thr Thr Thr Thr Trp Val Ala  
 260 265 270  
 Glu Asp Ala Gln Tyr Pro Ile Gly Asp Cys Gln Met Val Gly Ser Asn  
 275 280 285  
 Trp Val Asn Asn Asp Phe Ala Cys Asn Met Trp Asn Met Asp Glu Leu  
 290 295 300  
 Trp Gln Phe Ser Lys Leu Gln Lys  
 305 310

<210> 49  
 <211> 1186  
 <212> DNA  
 <213> Glycine max

<400> 49  
 aattcggcac gaggccatgt ctacttcaaa gagcgtcagc agttctagtg aagatgacaa 60  
 tgaacttaga agagggcctt ggactcttga agaggataat ttgctctccc aatataatttc 120  
 tagtcatgga gaagggcgat ggaatttgct agctaaacgt tcaggattaa agcgaactgg 180  
 gaaaagttgc agattaaggt ggctaaatta tctaaagcca gatgtaaaac ggggaaattt 240  
 aacccccaaa gagcaactta taatcctcga actccactca aagtggggaa acaggtgggtc 300  
 aaaaattgca caaaatttgc caggcagaac agacaatgaa atcaagaact attggagaac 360  
 taggattcag aaacaagcaa gacatttgaa aattgacact gacaccagag agtttcagga 420  
 acttgttagg cgtttctgga tgcctagatg cttcaaaaag cccaagaatc atcttcttca 480  
 gccatgtcaa ttcaaaacca ggcaactcct atgccttttg atggtgtttc tcagcattca 540  
 actggtggga ccataccatc acattcacac accccttggc agggaccttg tatgaatgaa 600  
 gctgggtccca cttacatgga ccaacatgag cagaactcag actctgaaca caacaatggg 660  
 tcatgcatct ccttgtctga gtcagcaaat tttccaaaag tgcctcagca ttttggaagc 720  
 accaccatca cccaatatca tgccttgaat aacaatgact ttggcacctt cacatatgac 780  
 ggctacaatg taagcaacaa tgtctatgag atggacaact tcaaaacgcc tactacaagg 840  
 gtggctgagg atgcgcaata cccaactggg gattgtcaaa tggtaggaag caattgggta 900

aacagcgaatt ttgcatgtaa catgtggaac atggatgaat tgtggcaatt tagcaagtta 960  
 caaaaataag attttagggt ttgggttttt ttggagttacc aagactctat ctttgggtgat 1020  
 gttattattg ttatcatgaa ctgttgatta gctactacca aattaattaa tacagatggg 1080  
 gattgttttc tgtacatctg ttttgcatc ctctgttttg caatttgat tgattgagaa 1140  
 aagtcattaa ttagtcacta gttcaaaaca caaaaaaaaa aaaaaa 1186

<210> 50  
 <211> 192  
 <212> PRT  
 <213> Glycine max

<400> 50  
 Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu  
 1 5 10 15  
 Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln  
 20 25 30  
 Tyr Ile Ser Ser His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg  
 35 40 45  
 Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn  
 50 55 60  
 Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln  
 65 70 75 80  
 Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys  
 85 90 95  
 Ile Ala Gln Asn Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
 100 105 110  
 Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Asp Thr  
 115 120 125  
 Asp Thr Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg  
 130 135 140  
 Cys Phe Lys Lys Pro Lys Asn His Leu Leu Gln Pro Cys Gln Phe Lys  
 145 150 155 160  
 Thr Arg Gln Leu Leu Cys Leu Leu Met Val Phe Leu Ser Ile Gln Leu  
 165 170 175  
 Leu Gly Pro Tyr His His Ile His Thr Pro Leu Gly Arg Asp Leu Val  
 180 185 190

<210> 51  
 <211> 487  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (358)

<220>  
 <221> unsure  
 <222> (429)

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<400> 51
gagaaataaa aagagaagaa agaaaacacg atagtatcat catatcacca ccacacacat 60
agatagagag aggaaaacga cctatatattt ttttcctttg agagcttcag gggctaggaa 120
aattagaagg acagccacaa gtataaaggc ggtgaaataa aagagaaaga caagaaggag 180
acatgggaag accaccttgt tgtgacaaag aaggggtcaa gaaagggcct tggactcctg 240
aagaagacat catattgggtg tcttatattc aggaacatgg tcctggaaat tggagggcag 300
ttcctgccaa aacaggggttg tcaagatgca gcaagagttg cagacttaga tggacgantt 360
acctgaggcc aggaatcaag cgtggtaact tcacaagaac aagaggagaa gatgataatc 420
catcttcang atcttttagg aaacagatgg ggtgcaatag cttcatacct tccacaaagg 480
acaaggg
487

```

```

<210> 52
<211> 90
<212> PRT
<213> Glycine max

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<220>
<221> UNSURE
<222> (59)

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```

<220>
<221> UNSURE
<222> (72)

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```

<220>
<221> UNSURE
<222> (83)

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<400> 52
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
 1          5          10          15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
      20          25          30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
      35          40          45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Xaa Tyr Leu Arg Pro Gly
      50          55          60

Ile Lys Arg Gly Asn Phe Thr Xaa Glu Gln Glu Glu Lys Met Ile Ile
      65          70          75          80

His Leu Xaa Asp Leu Leu Gly Asn Arg Trp
      85          90

```

```

<210> 53
<211> 1556
<212> DNA
<213> Glycine max

```

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<400> 53
gcacgaggag aaataaaaag agaagaaaga aaacacgata gtatcatcat atcaccacca 60
cacacataga tagagagagg aaaacgacct atatattttt tcctttgaga gcttcagggg 120
ctaggaaaat tagaaggaca gccacaagta taaaggcggt gaaataaaaag agaaagacaa 180
gaaggagaca tgggaagacc accttggtgtg gacaaagaag gggccaagaa agggccttgg 240
actcctgaag aagacatcat attggtgtct tatattcagg aacatgggtcc tggaaattgg 300
agggcagttc ctgccaaaac agggttgtca agatgcagca agagttgcag acttagatgg 360

```

```

acgaattacc tgaggccagg aatcaagcgt ggtaacttca cagaacaaga ggagaagatg 420
ataatccatc ttcaagatct tttaggaaac agatgggctg caatagcttc ataccttcca 480
caaagaacag acaatgacat aaagaactat tggaataccc atttgagaaa gaagctgaag 540
aagatgcaag caggcggtag aggtggtagc tttggagaag ggttttcagc ctcaaggcaa 600
atccctagag gccagtggga aagaaggctc caaactgata tccaaatggc aaagagagcc 660
ctcagtgaag ctctttcacc agagaaaaag ccattctgtt tatctgcctc aaactcaaac 720
ccttcagata gtagcagctc cttctcttcc acaaaaccaa caacaacaca atctgtgtgc 780
tatgcatcaa gtgctgacaa catagctaga atgctcaagg gttggatgaa gaaccaccca 840
aagtcctcaa gaaccaactc gtctatgact cagaactcat tcaacaactt agcagggtgct 900
gatactgctt gtagtagtgg agcaaaggga ccactaagca gtgccgaatt gtctgagaat 960
aattttgaat ccttggttga ttttgatcag tcttgaggag cttcaaactc tgatcaattc 1020
tctcagtcct tgtctcctga ggccactgtt ttgcaagatg aaagcaagcc tgatattaat 1080
attgctgcag aaattatgcc cttctctttg cttgagaaat ggctccttga tgaggcagg 1140
tgccaagaga aattagtgtg ttgttgtggt gatgccaagt ttttctaagt tgggttcatt 1200
ttgtgacata tgagactgtg ggattttttt attttatttt attttatttc ataagttata 1260
ggtagggcct catcaattaa tctcgcttcg gccttattag agagagaagt tttccagcct 1320
ttgggtgctag acgtgtatat gttaattatt attgacatta tgatgattat tatcatactg 1380
tgttagtgtc catacactgg caaacttgct tctcttatgt aaagttgatc ttgcgacgag 1440
atcctgcttt atggctttag gcagcgcgac cgggtcttct tctttgtgtc gcttgattag 1500
taaccccccc cggggggggc ccgggtccaa atcccccccta atgggggtcct ttttag 1556

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<210> 54
<211> 332
<212> PRT
<213> Glycine max

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<400> 54
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
 1          5          10          15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
          20          25          30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
          35          40          45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
          50          55          60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Met Ile Ile His
          65          70          75          80

Leu Gln Asp Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
          85          90          95

Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
          100          105          110

Arg Lys Lys Leu Lys Lys Met Gln Ala Gly Gly Glu Gly Gly Ser Phe
          115          120          125

Gly Glu Gly Phe Ser Ala Ser Arg Gln Ile Pro Arg Gly Gln Trp Glu
          130          135          140

Arg Arg Leu Gln Thr Asp Ile Gln Met Ala Lys Arg Ala Leu Ser Glu
          145          150          155          160

Ala Leu Ser Pro Glu Lys Lys Pro Ser Cys Leu Ser Ala Ser Asn Ser
          165          170          175

```

Asn Pro Ser Asp Ser Ser Ser Ser Phe Ser Ser Thr Lys Pro Thr Thr  
 180 185 190  
 Thr Gln Ser Val Cys Tyr Ala Ser Ser Ala Asp Asn Ile Ala Arg Met  
 195 200 205  
 Leu Lys Gly Trp Met Lys Asn Pro Pro Lys Ser Ser Arg Thr Asn Ser  
 210 215 220  
 Ser Met Thr Gln Asn Ser Phe Asn Asn Leu Ala Gly Ala Asp Thr Ala  
 225 230 235 240  
 Cys Ser Ser Gly Ala Lys Gly Pro Leu Ser Ser Ala Glu Leu Ser Glu  
 245 250 255  
 Asn Asn Phe Glu Ser Leu Phe Asp Phe Asp Gln Ser Leu Glu Ser Ser  
 260 265 270  
 Asn Ser Asp Gln Phe Ser Gln Ser Leu Ser Pro Glu Ala Thr Val Leu  
 275 280 285  
 Gln Asp Glu Ser Lys Pro Asp Ile Asn Ile Ala Ala Glu Ile Met Pro  
 290 295 300  
 Phe Ser Leu Leu Glu Lys Trp Leu Leu Asp Glu Ala Gly Cys Gln Glu  
 305 310 315 320  
 Lys Leu Val Gly Cys Cys Gly Asp Ala Lys Phe Phe  
 325 330

<210> 55  
 <211> 357  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (259)

<220>  
 <221> unsure  
 <222> (307)

<220>  
 <221> unsure  
 <222> (319)

<400> 55  
 gccaaagtat caggtttgag ggggtgggga tccaaaaatt aggtagctat attgaagtat 60  
 ttgcgcaaaa gtcgcaacaa caaatgtcac ctttgctaata aactttcttc ttgcttcaac 120  
 ctctgtaatc tccatgcagg cctcaaccgc acaggaaaga gctgtgcgct ccggtgggtt 180  
 aactacctcc accctgggcc taaagcgtgg gcgcatgact ccccatgaaa gaacgcctca 240  
 tcctccaact ccatgctcng tggggaaaca agtgggtccaa ggataacacg gaactgccaa 300  
 ggcgtancca caatgaatna aagaactact gggagaacac atttgaggaa aaggaag 357

<210> 56  
 <211> 54  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (21)

<220>  
 <221> UNSURE  
 <222> (27)..(28)

<220>  
 <221> UNSURE  
 <222> (41)

<400> 56  
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn  
     1                    5                    10                    15  
 Tyr Leu His Pro Xaa Leu Lys Arg Gly Arg Xaa Xaa Pro Met Lys Glu  
                     20                    25                    30  
 Arg Leu Ile Leu Gln Leu His Ala Xaa Trp Gly Asn Lys Trp Ser Lys  
             35                    40                    45  
 Asp Asn Thr Glu Leu Pro  
     50

<210> 57  
 <211> 1072  
 <212> DNA  
 <213> Triticum aestivum

<400> 57  
 gcacgaggcc aaagtatcag gtttgagggg tgggggatcc aaaaattagg tagctatatatt 60  
 gaagtatttt gcgcaaagtc gcaacaacaa atgtcacctt tgctaataac tttcttcttg 120  
 cttcaacctc tgtaatctcc atgcaggcct caaccgcaca ggaaagagct gtcgcctccg 180  
 gtgggttaac tacctccacc ctggcctaaa gcgtggggcg atgactcccc atgaagaacg 240  
 cctcatcctc gagctccatg ctcggtgggg aaacaggtgg tccaggatag cacggaagct 300  
 gccaggggcg accgacaatg agatcaagaa ctactggaga acacatatga ggaagaaagc 360  
 acaggagagg aagaggagcg tgtcaccctc accatcttca tcctcagtga cataccaatc 420  
 cattcagcca cagacgccat cgatcatggg aattggcgag caggaacttc atggtggcag 480  
 tagctgcatc acaagcatat tgaagggcac gcctgctgac atggatggat acctcatgga 540  
 tcagatatgg atggagattg aggcaccctc tgggggtcaac tttcatgacg ggaaggataa 600  
 ttcatacagc agcccctctg gccctctgct gccatcaccg atgtgggatt actacagccc 660  
 tgaggcaggc tggaagatgg atgagataaa gatggcccca caagttagct acagtaaagg 720  
 aattggcccc agttattgaa gccatatata ttgtatcaga ttactaagtt acttgcaacc 780  
 tagcagaagt gaaatgcttt tggtgaaaga accattagca tggatctaaa aaatatattat 840  
 atctatctag cattccaagt gtgctcatgt tttatgtatc tactatgtag catctagtgt 900  
 gcaagacatg taatgcaagg acacttccac tttgtattca caataatcag ctatctcctg 960  
 taagactttt ccaatgcaaa catgattagc aggtgtaata tcaacttaaa tgcttgccaa 1020  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1072

<210> 58  
 <211> 198  
 <212> PRT  
 <213> Triticum aestivum

<400> 58  
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn  
     1                    5                    10                    15



Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Thr Pro His Glu Glu  
                   20                  25                  30  
 Arg Leu Ile Leu Glu Leu His Ala Arg Trp Gly Asn Arg Trp Ser Arg  
                   35                  40                  45  
 Ile Ala Arg Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
           50                  55                  60  
 Trp Arg Thr His Met Arg Lys Lys Ala Gln Glu Arg Lys Arg Ser Val  
   65                  70                  75                  80  
 Ser Pro Ser Pro Ser Ser Ser Ser Val Thr Tyr Gln Ser Ile Gln Pro  
                   85                  90                  95  
 Gln Thr Pro Ser Ile Met Gly Ile Gly Glu Gln Glu Leu His Gly Gly  
                   100                  105                  110  
 Ser Ser Cys Ile Thr Ser Ile Leu Lys Gly Thr Pro Ala Asp Met Asp  
           115                  120                  125  
 Gly Tyr Leu Met Asp Gln Ile Trp Met Glu Ile Glu Ala Pro Ser Gly  
   130                  135                  140  
 Val Asn Phe His Asp Gly Lys Asp Asn Ser Tyr Ser Ser Pro Ser Gly  
  145                  150                  155                  160  
 Pro Leu Leu Pro Ser Pro Met Trp Asp Tyr Tyr Ser Pro Glu Ala Gly  
                   165                  170                  175  
 Trp Lys Met Asp Glu Ile Lys Met Ala Pro Gln Val Ser Tyr Ser Lys  
           180                  185                  190  
 Gly Ile Gly Pro Ser Tyr  
           195

<210> 59  
 <211> 521  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (108)

<220>  
 <221> unsure  
 <222> (355)

<220>  
 <221> unsure  
 <222> (361)

<220>  
 <221> unsure  
 <222> (392)

<220>  
 <221> unsure  
 <222> (414)

<220>  
 <221> unsure  
 <222> (431)

<220>  
 <221> unsure  
 <222> (434)

<220>  
 <221> unsure  
 <222> (447)

<220>  
 <221> unsure  
 <222> (456)

<220>  
 <221> unsure  
 <222> (459)

<400> 59  
 cttggatcct ccactagcta cgtcgtccat ggatgtggtg ctgcagagtc gtagcagcaa 60  
 cagcatggcg gcggagccgg aggaggaggc ggaccggagg aggaggcngg agctccggcg 120  
 agggccgtgg acggtggacg aggaccttac gctgatcaac tacatcgcg accacggcga 180  
 gggccgctgg aacgcgctgg cgcgggccgc cggcctgagg cgcacgggga agagctgccg 240  
 gctgcggtgg ctgaactacc tccgccccga cgtgaagcgc ggcaacttca ccgccgacga 300  
 gcagctcctc atcctcgacc tccactctcg ctggggcaac cgggtggtcg agatngcgca 360  
 ncacctcccg ggtcggacgg acaacgaaga tnaaagaact actgggagga ccanggtgca 420  
 aaaagcacgc naancaactc aactgcnaac tccggnanc gcaaccttta aaggatgcca 480  
 ataaggtacc tctggatgcc tcgcctctca acgcatcaac c 521

<210> 60  
 <211> 131  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (27)

<220>  
 <221> UNSURE  
 <222> (109)

<220>  
 <221> UNSURE  
 <222> (111)

<220>  
 <221> UNSURE  
 <222> (122)

<220>  
 <221> UNSURE  
 <222> (129)

<400> 60  
 Met Asp Val Val Leu Gln Ser Arg Ser Ser Asn Ser Met Ala Ala Glu  
 1 5 10 15

Pro Glu Glu Glu Ala Asp Arg Arg Arg Arg Xaa Glu Leu Arg Arg Gly  
                   20                                  25                                  30  
 Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Ile Asn Tyr Ile Ala Asp  
                   35                                  40                                  45  
 His Gly Glu Gly Arg Trp Asn Ala Leu Ala Arg Ala Ala Gly Leu Arg  
                   50                                  55                                  60  
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro  
                   65                                  70                                  75                                  80  
 Asp Val Lys Arg Gly Asn Phe Thr Ala Asp Glu Gln Leu Leu Ile Leu  
                                   85                                  90                                  95  
 Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser Lys Xaa Ala Xaa His  
                                  100                                 105                                 110  
 Leu Pro Gly Arg Thr Asp Asn Glu Asp Xaa Arg Thr Thr Gly Arg Thr  
                  115                                 120                                 125  
 Xaa Val Gln  
                  130

<210> 61  
 <211> 464  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (435)

<220>  
 <221> unsure  
 <222> (442)

<220>  
 <221> unsure  
 <222> (450)

<220>  
 <221> unsure  
 <222> (457)

<400> 61  
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 ggcccctgga cgccggagga ggacctcgtg ctcgctctcct acgtccagga gcacggcccc 120  
 ggcaactggc gcgcggtccc caccaggacc ggctgatgc ggtgtagcaa gagctgccgg 180  
 ctccggtgga ccaactacct gcgcccaggg atcaagcgcg gcaacttcac cgaccaggag 240  
 gagaagctca tcgtccacct ccaggcgctg ctcggaaca ggtgggccgc gatcgctctc 300  
 tacctccccg agcgcaccca caacgacatc aagaactact ggaacacgca actcaagcgc 360  
 aagctgcaag cggggggcga cgccgcgggc aaaccggcgg cgcaaaggct gctcctcctc 420  
 aaagggcaat ggganaggcg gngcagacgn catcaanatg cgcc 464

<210> 62  
 <211> 122  
 <212> PRT  
 <213> Triticum aestivum

<400> 62  
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro  
1 5 10 15  
Trp Thr Pro Glu Glu Asp Leu Val Leu Val Ser Tyr Val Gln Glu His  
20 25 30  
Gly Pro Gly Asn Trp Arg Ala Val Pro Thr Arg Thr Gly Leu Met Arg  
35 40 45  
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
50 55 60  
Ile Lys Arg Gly Asn Phe Thr Asp Gln Glu Glu Lys Leu Ile Val His  
65 70 75 80  
Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu  
85 90 95  
Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Gln Leu  
100 105 110  
Lys Arg Lys Leu Gln Ala Gly Gly Asp Ala  
115 120

<210> 63  
<211> 217  
<212> PRT  
<213> Pisum sativum

<400> 63  
Met Asp Lys Lys Pro Cys Asn Ser Ser Gln Asp Pro Glu Val Arg Lys  
1 5 10 15  
Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala  
20 25 30  
Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu  
35 40 45  
Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg  
50 55 60  
Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile  
65 70 75 80  
Met Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys  
85 90 95  
His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr  
100 105 110  
Arg Ile Gln Lys His Ile Lys Gln Val Asp Asn Pro Asn Gln Gln Asn  
115 120 125  
Phe Gln Gln Lys Met Ser Leu Glu Ile Asn Asp His His His His His  
130 135 140

Pro	His	Gln	Pro	Ser	Ser	Ser	Gln	Val	Ser	Asn	Leu	Val	Glu	Pro	Met
145					150					155					160
Glu	Thr	Tyr	Ser	Pro	Thr	Ser	Tyr	Gln	Gly	Thr	Leu	Glu	Pro	Phe	Pro
				165					170					175	
Thr	Gln	Phe	Pro	Thr	Ile	Asn	Asn	Asp	His	His	Gln	Asn	Ser	Asn	Cys
			180					185					190		
Cys	Ala	Asn	Asp	Asn	Asn	Asn	Asn	Asn	Tyr	Trp	Ser	Met	Glu	Asp	Ile
	195						200					205			
Trp	Ser	Met	Gln	Leu	Leu	Asn	Gly	Asp							
210						215									